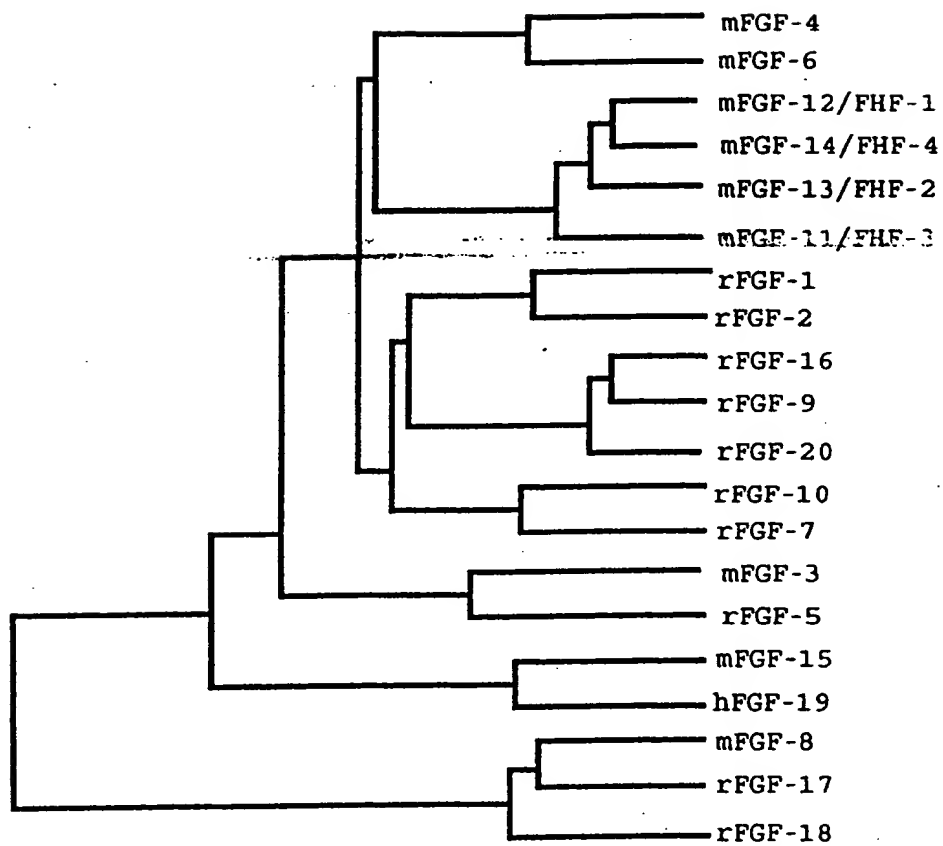


Figure 1

rat FGF-9	MAPLGEVGSYF-GVQI)-AVPFGNVPVL--PVDSPVLLSDHLGQSEAGGLPRGPAVTDLDHL	57
	**** *	
rat FGF-20	MAPLTEVGAFLLGGLGLGQVGSFLLPPAGERPPLLGERGALL-RGARGPGGSVELAHL	60
	*** *	
rat FGF-16	MAEVGGVFASLDWDLQGFSSSLGNVPLADSPGLNERLGQIE--GKLQRGSPTDFAHL	96
	KGILRRRQLYCRTGFYLEIFPNGTIQGRKDHRSRFGILEFISIAVGLVSIRGVDSGLYLG	117
	***** *	
	HGILRRRQLYCRTGFILQILPDGSVQGRQDHSLSFGILEFISIAVGLVSIRGVDSGLYLG	120
	***** *	
	KGILRRRQLYCRTGFHLEIFPNGTVHGTRHDHSRFGILEFISIAVGLVSIRGVDSGLYLG	116
	MNEKGELYGSEKLTQECVFRQFEENWYNTYSSNL YKHVDTRRRYYVALNKDGTREGTR	177
	** ***** *	
	MNGKGELYGSEKLTSCIFRQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTREGAR	180
	** ***** *	
	MNERGELFGSKKLTRECVFRQFEENWYNTYASTLYKHSDSERQYVALNKDGSREGYR	176
	TKRHQKFTHFLPRPVI:PDKVPELYKDILSQS	208
	***** *	
	SKRHQKFTHFLPRPVI:PERVPELYKOLLVYTG	212
	***** *	
	TKRHQKFTHFLPRPVDPSKLPMSRDLFRYR	207



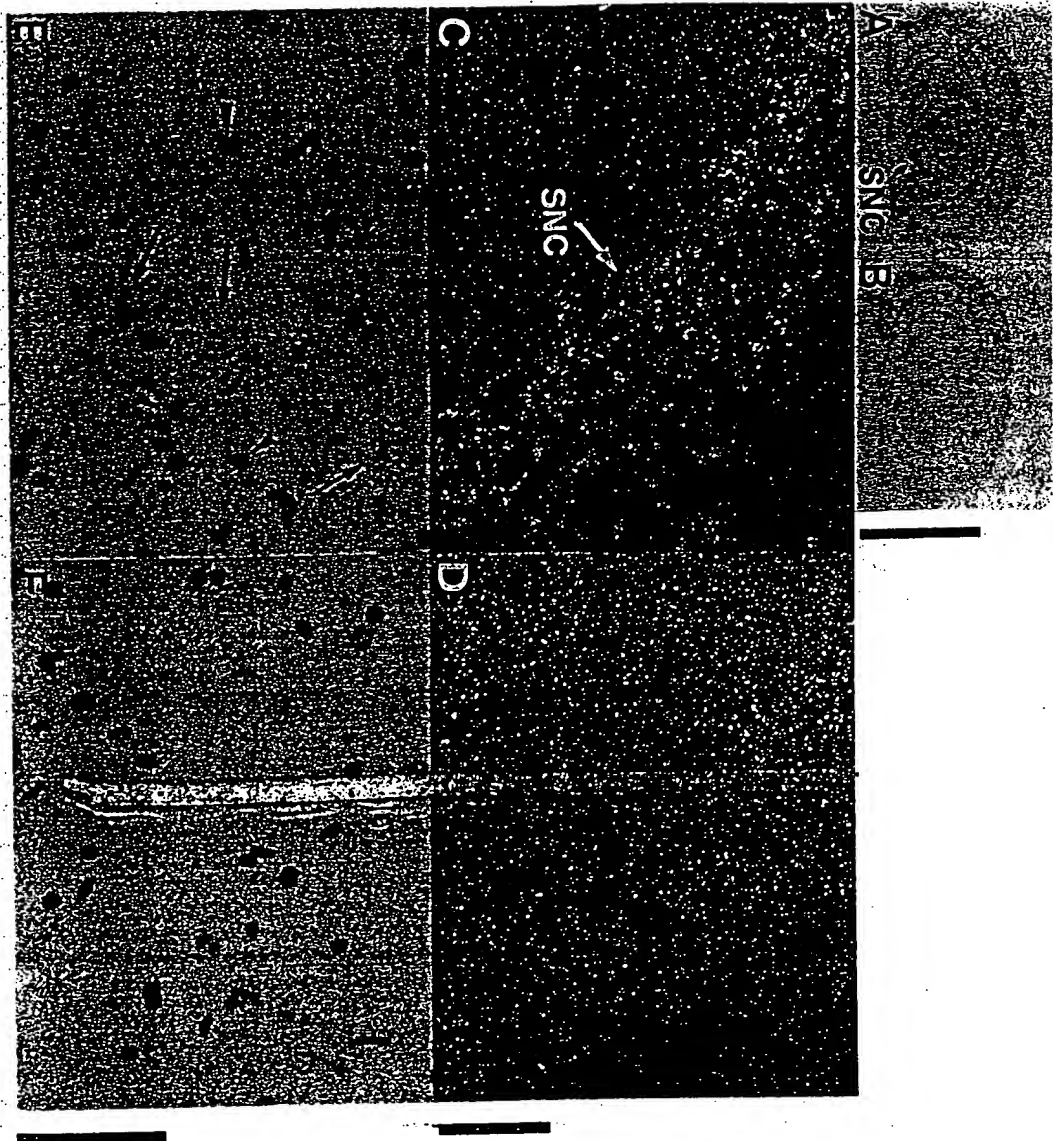
*Figure 2*



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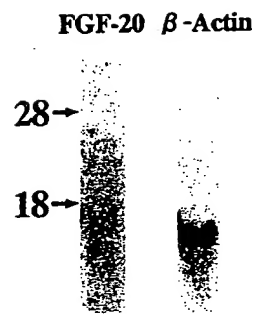
Figure 3



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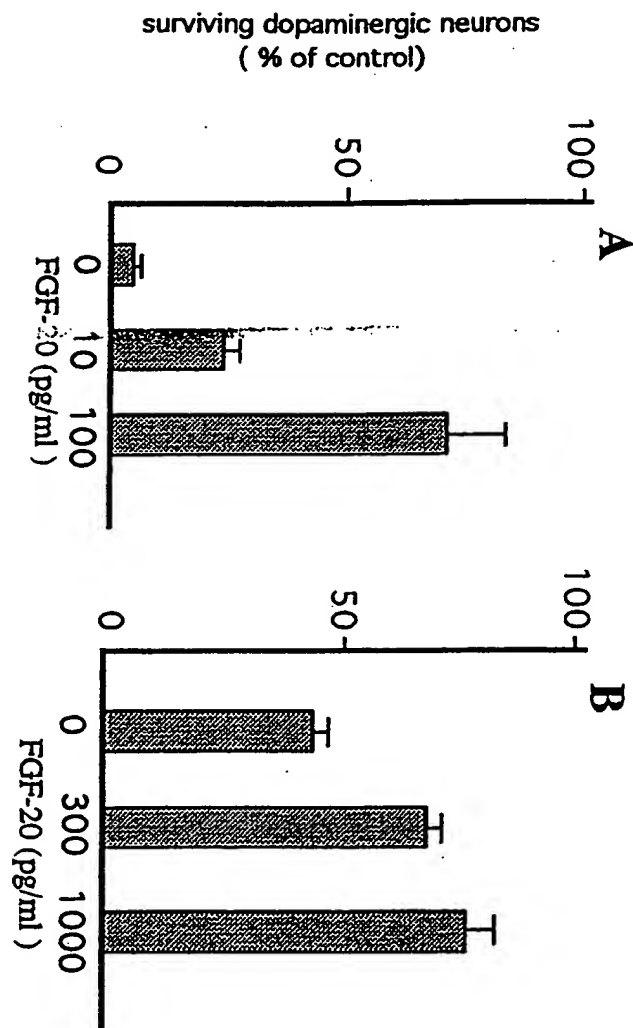
**Figure 4**



000000T" 54626960



**Figure 5**



091692945 .102000



## Figure 6

SEQ ID NO:1

Rat FGF-20 DNA

Translation start and stop codons indicated in bold, underlined type.

CCTTCCATGGCTCCCTTGACCGAAGTCGGTGCCTTCTTGGGCGGCCTGGAGGGCTTGGGCCAGCAGGTGGGG  
TCGCACTTCTTGCTGCCTCCTGCAGGGGAGCGACCGCCGCTGCTAGGGGAGCGGCGGGGCGGTTGGAGCGG  
GGCGCCCGCGGGCGGGCCGGGTTCCGTGGAGCTGGCGCACCTGCACGGCATCCTGCGCCGCGGCAGCTCTAC  
TGCCGCACCGGCTTCCACCTGCAGATCCTGCCCCACGGCAGTGTGCAGGGCACCCGGCAGGATCACAGCCTC  
TTCGGTATCCTGGAATTCATCAGTGTGGCGGTGGGGCTGGTCAGTATCAGAGGTGTGGACAGCGGCCTGTAC  
CTTGGCATGAATGGCAAAGGAGAGCTTTATGGCTCAGAGAAATTGACTTCTGAATGCATCTTCAGGGAACAA  
TTTGAAGAGAAGTGGTATAATACCTATTTCATCCAACATATACAAACACGGAGACACAGGTTCGAGGTATTTT  
GTAGCACTTAACAAAGACGGGACTCCAAGGGACGGTGCCAGGTCCAAAAGACACCAAAAGTTTACCCATTTT  
TTACCCAGACCAGTGGACCCAGAGAGAGTCCCAGAGTTATACAAAGACCTACTGGTGTACACTGGATGAACC

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## Figure 7

SEQ ID NO:2

Amino acid sequence of rat FGF-20

MAPLTEVGAFLGGLEGLGQQVGSFLLPPAGERPPLLGERRGALERGARGGPGSVELAHLHGILRRRQLYCR  
TGFHLQILPDGSVQGTRQDHSLEFGILEFISVAVGLVSIRGVDSGLYLG MNGKGELYGSEKLTSECIFREQFE  
ENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGARSKRHQKFTHFLPRPVDPERVPELYKDLLVYTG

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# Figure 8

humanFGF-20 DNA (coding)

Sequence Size : 636

```

      10      20      30      40      50      60
atggctcccttagccgaagtcgggggctttctgggcggcctggagggcttgggccagcag
M A P L A E V G G F L G G L E G L G Q Q

      70      80      90     100     110     120
gtgggttcgcatttcctgttgccctcctgccggggagcggccgctgctgggcgagcgc
V G S H F L L P P A G E R P P L L G E R

      130     140     150     160     170     180
aggagcgcggcggagcggagcgcgcgcggcggggcggggctgcgcagctggcgcacctg
R S A A E R S A R G G P G A A Q L A H L

      190     200     210     220     230     240
cacggcctcctgcgccgcggcagctctattgccgcaccggcttcacactgcagatcctg
H G I L R R R Q L Y C R T G F H L Q I L

      250     260     270     280     290     300
cccgacggcagcgtgcagggcacccggcaggaccacagcctcttcggtatcttgaattc
P D G S V Q G T R Q D H S L F G I L E F

      310     320     330     340     350     360
atcagtgtggcagtgaggactggtcagtaggtgtggacagtggtctctatcttga
I S V A V G L V S I R G V D S G L Y L G

      370     380     390     400     410     420
atgaatgacaaaggagaactctatggatcagagaaacttacttccgaatgcacatcttagg
M N D K G E L Y G S E K L T S E C I F R

      430     440     450     460     470     480
gagcagtttgaagagaactggtataacacctattcatctaacaatataaacaatggagac
E Q F E E N W Y N T Y S S N I Y K H G D

      490     500     510     520     530     540
actggccgcaggtattttgtggcacttaacaaagacggaactccaagagatggcgccagg
T G R R Y F V A L N K D G T P R D G A R

      550     560     570     580     590     600
tccaagaggcatcagaaatttacacatttcttacctagaccagtggatccagaaagagtt
S K R H Q K F T H F L P R P V D P E R V

      610     620     630     640
ccagaattgtacaaggacactgatgtacattga
P E L Y K D L L M Y T *

```

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Figure 9

rat FGF-20	MAPL	TEVGAFLGGLEGLGQQVGS	HFLPPAGERPPLL	GERRGALERGARGGPGS	VELAHL	60
	***	***	*****	*****	*****	***
human FGF-20	MAPL	AEVGGFLGGLEGLGQQVGS	HFLPPAGERPPLL	GERRSAAERSARGGPGAAQ	LAHL	60
	HGIL	RRRQLYCRTGFHLQILPDG	SVQGT	RQDHS	LFGILEFISVAVGLVSIRGV	DSGLYLG
	*****	*****	*****	*****	*****	*****
	HGIL	RRRQLYCRTGFHLQILPDG	SVQGT	RQDHS	LFGILEFISVAVGLVSIRGV	DSGLYLG
	*****	*****	*****	*****	*****	*****
	MNGK	GELYGSEKLTSECI	FREQFEENWYNTYSSNIYKH	GDTGRRYFVALNKDGT	PRDGAR	180
	**	*****	*****	*****	*****	*****
	MNDK	GELYGSEKLTSECI	FREQFEENWYNTYSSNIYKH	GDTGRRYFVALNKDGT	PRDGAR	180
	SKRHQK	FTHFLPRPVDPERVPELYK	DLLVYT	G		212
	*****	*****	*****	*****	*****	**
	SKRHQK	FTHFLPRPVDPERVPELYK	DLLMYT			211



**Figure 10**

Codon usage for enteric bacterial (highly expressed) genes 7/19/83

AmAcid	Codon	Number	/1000	Fraction
Gly	GGG	13.00	1.89	0.02
Gly	GGA	3.00	0.44	0.00
Gly	GGU	365.00	52.99	0.59
Gly	GGC	238.00	34.55	0.38
Glu	GAG	108.00	15.68	0.22
Glu	GAA	394.00	57.20	0.78
Asp	GAU	149.00	21.63	0.33
Asp	GAC	298.00	43.26	0.67
Val	GUG	93.00	13.50	0.16
Val	GUA	146.00	21.20	0.26
Val	GUU	289.00	41.96	0.51
Val	GUC	38.00	5.52	0.07
Ala	GCG	161.00	23.37	0.26
Ala	GCA	173.00	25.12	0.28
Ala	GCU	212.00	30.78	0.35
Ala	GCC	62.00	9.00	0.10
Arg	AGG	1.00	0.15	0.00
Arg	AGA	0.00	0.00	0.00
Ser	AGU	9.00	1.31	0.03
Ser	AGC	71.00	10.31	0.20
Lys	AAG	111.00	16.11	0.26
Lys	AAA	320.00	46.46	0.74
Asn	AAU	19.00	2.76	0.06
Asn	AAC	274.00	39.78	0.94
Met	AUG	170.00	24.68	1.00
Ile	AUA	1.00	0.15	0.00
Ile	AUU	70.00	10.16	0.17
Ile	AUC	345.00	50.09	0.83
Thr	ACG	25.00	3.63	0.07
Thr	ACA	14.00	2.03	0.04





AmAcid	Codon	Number	/1000	Fraction
Thr	ACU	130.00	18.87	0.35
Thr	ACC	206.00	29.91	0.55
Trp	UGG	55.00	7.98	1.00
End	UGA	0.00	0.00	0.00
Cys	UGU	22.00	3.19	0.49
Cys	UGC	23.00	3.34	0.51
End	UAG	0.00	0.00	0.00
End	UAA	0.00	0.00	0.00
Tyr	UAU	51.00	7.40	0.25
Tyr	UAC	157.00	22.79	0.75
Leu	UUG	18.00	2.61	0.03
Leu	UUA	12.00	1.74	0.02
Phe	UUU	51.00	7.40	0.24
Phe	UUC	166.00	24.10	0.76
Ser	UCG	14.00	2.03	0.04
Ser	UCA	7.00	1.02	0.02
Ser	UCU	120.00	17.42	0.34
Ser	UCC	131.00	19.02	0.37
Arg	CGG	1.00	0.15	0.00
Arg	CGA	2.00	0.29	0.01
Arg	CGU	290.00	42.10	0.74
Arg	CGC	96.00	13.94	0.25
Gln	CAG	233.00	33.83	0.86
Gln	CAA	37.00	5.37	0.14
His	CAU	18.00	2.61	0.17
His	CAC	85.00	12.34	0.83
Leu	CUG	480.00	69.69	0.83
Leu	CUA	2.00	0.29	0.00
Leu	CUU	25.00	3.63	0.04
Leu	CUC	38.00	5.52	0.07
Pro	CCG	190.00	27.58	0.77
Pro	CCA	36.00	5.23	0.15
Pro	CCU	19.00	2.76	0.08
Pro	CCC	1.00	0.15	0.00

[illegible]



# Figure 11

Codon usage for yeast (highly expressed) genes

AmAcid	Codon	Number	/1000	Fraction	..
Gly	GGG	33.00	0.86	0.01	
Gly	GGA	70.00	1.82	0.02	
Gly	GGT	2672.00	69.62	0.91	
Gly	GGC	171.00	4.46	0.06	
Glu	GAG	277.00	7.22	0.10	
Glu	GAA	2442.00	63.63	0.90	
Asp	GAT	1100.00	28.66	0.48	
Asp	GAC	1211.00	31.55	0.52	
Val	GTG	117.00	3.05	0.04	
Val	GTA	75.00	1.95	0.03	
Val	GTT	1548.00	40.33	0.56	
Val	GTC	1026.00	26.73	0.37	
Ala	GCG	36.00	0.94	0.01	
Ala	GCA	203.00	5.29	0.06	
Ala	GCT	2221.00	57.87	0.65	
Ala	GCC	969.00	25.25	0.28	
Arg	AGG	20.00	0.52	0.01	
Arg	AGA	1336.00	34.81	0.83	
Ser	AGT	116.00	3.02	0.05	
Ser	AGC	94.00	2.45	0.04	
Lys	AAG	2365.00	61.62	0.78	
Lys	AAA	651.00	16.96	0.22	
Asn	AAT	347.00	9.04	0.22	
Asn	AAC	1259.00	32.80	0.78	
Met	ATG	766.00	19.96	1.00	
Ile	ATA	43.00	1.12	0.02	
Ile	ATT	1223.00	31.87	0.52	
Ile	ATC	1070.00	27.88	0.46	

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*Figure 11 (continued)*

Pro	CCG	10.00	0.26	0.01
Pro	CCA	1271.00	33.12	0.80
Pro	CCT	279.00	7.27	0.18
Pro	CCC	33.00	0.86	0.02

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## Figure 12

Codon usage for *Drosophila* (highly expressed) genes

AmAcid	Codon	Number	/1000	Fraction	..
Gly	GGG	6.00	0.28	0.00	
Gly	GGA	380.00	18.04	0.22	
Gly	GGT	575.00	27.29	0.34	
Gly	GGC	746.00	35.41	0.44	
Glu	GAG	1217.00	57.77	0.91	
Glu	GAA	115.00	5.46	0.09	
Asp	GAT	503.00	23.88	0.43	
Asp	GAC	654.00	31.04	0.57	
Val	GTG	719.00	34.13	0.45	
Val	GTA	29.00	1.38	0.02	
Val	GTT	226.00	10.73	0.14	
Val	GTC	608.00	28.86	0.38	
Ala	GCG	94.00	4.46	0.05	
Ala	GCA	80.00	3.80	0.04	
Ala	GCT	446.00	21.17	0.24	
Ala	GCC	1277.00	60.61	0.67	
Arg	AGG	48.00	2.28	0.06	
Arg	AGA	12.00	0.57	0.01	
Ser	AGT	16.00	0.76	0.01	
Ser	AGC	267.00	12.67	0.23	
Lys	AAG	1360.00	64.55	0.93	
Lys	AAA	108.00	5.13	0.07	
Asn	AAT	127.00	6.03	0.13	
Asn	AAC	878.00	41.67	0.87	
Met	ATG	387.00	18.37	1.00	
Ile	ATA	4.00	0.19	0.00	
Ile	ATT	390.00	18.51	0.29	
Ile	ATC	969.00	45.99	0.71	

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*Figure 12 (continued)*

Thr	ACG	114.00	5.41	0.08
Thr	ACA	34.00	1.61	0.02
Thr	ACT	164.00	7.78	0.11
Thr	ACC	1127.00	53.49	0.78
Trp	TGG	243.00	11.53	1.00
End	TGA	1.00	0.05	0.01
Cys	TGT	20.00	0.95	0.08
Cys	TGC	220.00	10.44	0.92
End	TAG	12.00	0.57	0.17
End	TAA	58.00	2.75	0.82
Tyr	TAT	113.00	5.36	0.16
Tyr	TAC	574.00	27.25	0.84
Leu	TTG	210.00	9.97	0.12
Leu	TTA	9.00	0.43	0.01
Phe	TTT	62.00	2.94	0.09
Phe	TTC	635.00	30.14	0.91
Ser	TCG	195.00	9.26	0.17
Ser	TCA	29.00	1.38	0.02
Ser	TCT	103.00	4.89	0.09
Ser	TCC	558.00	26.49	0.48
Arg	CGG	7.00	0.33	0.01
Arg	CGA	25.00	1.19	0.03
Arg	CGT	281.00	13.34	0.34
Arg	CGC	465.00	22.07	0.55
Gln	CAG	703.00	33.37	0.91
Gln	CAA	66.00	3.13	0.09
His	CAT	88.00	4.18	0.22
His	CAC	312.00	14.81	0.78
Leu	CTG	1182.00	56.10	0.69
Leu	CTA	21.00	1.00	0.01
Leu	CTT	55.00	2.61	0.03
Leu	CTC	224.00	10.63	0.13

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